IN THE CLAIMS:

Applicant, pursuant to 37 C.F.R. § 1.121, submits the following amendments to the claims:

1. (Currently Amended) A method for analysis, diagnosis or prognosis of a cell proliferative disorder, comprising: ~~detecting the methylation state of the 5' and promoter region of the gene DD3 within a subject, said method comprising~~ contacting genomic DNA obtained from a test subject ~~a target nucleic acid comprising one or more sequences from the group of Seq. ID No.1 to Seq. ID No. 5 in a biological sample obtained from said subject~~ with at least one reagent or a series of reagents~~, wherein said reagent or series of reagents,~~ that distinguishes between methylated and non methylated CpG dinucleotides; and determining the methylation state of as least one CpG dinucleotide of SEQ ID NO:1, whereby a diagnosis or prognosis of a cell proliferative disorder is, at least in part, afforded ~~within the target nucleic acid~~.

2. (Currently amended) The method of claim 1, wherein determining the methylation state comprises analysis of at lease one sequence, or contiguous portion thereof, selected from the group consisting of SEQ ID NOS:2-5 ~~A method for the analysis of cell proliferative disorders, comprising: determination of the methylation state of one or more sequences from the group of Seq. ID No.1 to Seq. ID No. 5 according to Claim 1~~.

3. (Currently amended) The ~~A~~ method of ~~according to~~ Claim 1~~2~~, wherein the genomic DNA is obtained or derived from ~~biological sample is prostate cells or derived from~~ prostate cells.

4. (Currently amended) A nucleic acid molecule, comprising ~~a sequence~~ at least 18 contiguous bases of a sequence selected from the group consisting of SEQ ID NOS:1-5, ~~in length according to one of the sequences taken from the group comprising Seq. ID No. 1 to Seq. ID No. 5~~ and sequences complementary thereto.

5. (Currently amended) An oligomer~~, in particular an oligonucleotide~~ or peptide nucleic acid (PNA)-oligomer, ~~said oligomer in each case~~ consisting essentially of ~~at least one base sequence~~

~~having a length of~~ at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NOS:1-5, and sequences complimentary thereto ~~nucleotides which hybridises to or is identical to one of the nucleic acid sequences according to Seq. ID No. 1 to Seq. ID No. 5~~.

6. (Currently amended) The oligomer of claim 5, ~~An oligomer as recited in Claim 5~~, consisting essentially of a sequence selected from the group consisting of SEQ ID NOS:6-92 ~~one of the sequences taken from the group of Seq. ID No. 6 to Seq. ID No. 92~~.

7. (Currently amended) The oligomer of ~~as recited in~~ Claim 5, comprising ~~wherein the base sequence includes~~ at least one CpG dinucleotide.

8. (Currently amended) The oligomer of ~~as recited in~~ Claim 7, characterised in that the cytosine of the CpG dinucleotide is located approximately in the middle third of the oligomer.

9. (Currently amended) A set of oligomers, comprising at least two oligomers according to any one of claims 5 to 8.

10. (Currently amended) The ~~A~~ set of oligomers of ~~as recited in~~ Claim 9, comprising oligomers suitable for detecting the methylation state of all CpG dinucleotides within SEQ ID NO:1, ~~Seq. ID No. 1~~ and sequences complementary thereto.

11. (Currently amended) The ~~A~~ set of oligomers of claim 9, comprising oligomers suitable ~~at least two oligonucleotides as recited in one of Claims 5 to 10, which is used~~ as primer oligonucleotides for amplification of a sequence, or portion thereof, of a sequence selected from SEQ ID NOS:1-5, ~~the amplification of DNA sequences of one of Seq. ID No. 1 to Seq. ID No. 5~~ and sequences complementary thereto.

12. (Currently amended) The ~~A~~ set of oligonucleotides of claim 9, wherein ~~as recited in one of Claims 9 or 11, characterised in that~~ at least one oligonucleotide is bound to a solid phase.

13. (Currently amended) A method for determining methylation state of single nucleotide polymorphisms, comprising using ~~Use of~~ a set of oligonucleotides comprising at least three ~~of the~~ oligomers according to any one of claims 5 through 12 in at least one assay suitable for detecting at least one of a ~~the~~ cytosine methylation state, and a ~~and/or~~ single nucleotide polymorphisms (SNPs) within a sequence selected from the group consisting of SEQ ID NOS:1-5, ~~the sequences taken from the group of Seq. ID No. 1 to Seq. ID No. 5~~ and sequences complementary thereto.

14. (Cancelled) ~~A method for manufacturing an arrangement of different oligomers (array) fixed to a carrier material for analysing diseases associated with the methylation state of the CpG dinucleotides of the gene DD3, wherein at least one oligomer according to any of the claims 5 to 12 is coupled to a solid phase~~.

15. (Currently amended) An arrangement of different oligomers ~~(array)~~ according to any one of claims 5 through 12, coupled to a solid phase ~~obtainable according to claim 14~~.

16. (Currently amended) The array of claim 15, wherein the oligomers are ~~An array of different oligonucleotide- and/or PNA-oligomer sequences as recited in Claim 15, characterised in that these are~~ arranged ~~on a plane solid phase~~ in the form of a rectangular or hexagonal lattice.

17. (Currently amended) The array of claim 15, wherein the ~~as recited in any of the Claims 15 or 16, characterised in that the~~ solid phase comprises ~~surface is composed of~~ silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, ~~or~~ gold, and combinations thereof.

18. (Cancelled) ~~A DNA- and/or PNA-array for analysing diseases associated with the methylation state of the gene DD3 comprising at least one nucleic acid according to one of the preceding claims~~.

19. (Currently amended) A method for analysis, diagnosis or prognosis of a cell proliferative disorder, comprising: ~~A method for determining the methylation state within at least~~

~~one nucleic acid molecule according to one of Seq. ID No. 1 to Seq. ID No. 5, characterised in that the following steps are carried out:~~

a) obtaining, from a test subject, a biological sample containing genomic DNA,

b) isolating ~~extracting~~ the genomic DNA,

c) converting, by chemically treating the genomic DNA or a portion thereof, cytosine bases that ~~which~~ are unmethylated at the 5-position ~~within said DNA sample, by chemical treatment,~~ to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour;

d) amplifying ~~fragments of~~ the chemically pretreated genomic DNA, or a portion thereof, using a sets of primer oligonucleotides according to any one of Claims 11 or 12 and a polymerase~~,~~; and

e) ~~identifying~~ determining, based at least in part on the amplifying, the methylation status of one or more cytosine positions within a sequence selected from the group consisting of SEQ ID NOS:1-5, and sequences complementary thereto, whereby analysis, diagnosis or prognosis of a cell proliferative disorder is, at least in part, afforded.

20. (Currently amended) The method of claim 19, wherein determining in e) ~~as recited in Claim 19, characterised in that Step e)~~ is ~~carried out~~ by means of hybridisation of at least one oligonucleotide according to any one of Claims 5 to 12.

21. (Currently amended) The method of claim 19, wherein determining in e) ~~as recited in Claim 19, characterised in that Step e)~~ is ~~carried out~~ by means of hybridisation of at least one oligonucleotide according to any one of Claims 5 to 12, and extension of said hybridised oligonucleotide(s) by ~~means of~~ at least one nucleotide base.

22. (Currently amended) The method of claim 19, wherein determining in e) ~~as recited in Claim 19, characterised in that Step e)~~ is ~~carried out~~ by means of sequencing.

23. (Currently amended) The method of claim 19, wherein amplifying in d) ~~as recited in Claim 19, characterised in that Step d) is carried out using~~ comprises use of methylation specific primers.

24. (Currently amended) The method of claim 19, comprising ~~as recited in Claim 19, characterised in that Step e) is carried out by means of~~ a combination of at least two of the methods described in any one of Claims 20 to 23.

25. (Currently amended) The method of claim 19, wherein converting comprises use of an agent selected from the group consisting of as recited in Claim 19, characterised in that the chemical treatment is carried out by means of a solution of a bisulfite, hydrogen sulfite, ~~or~~ disulfite, and combinations thereof.

26. (Currently amended) A method for analysis, diagnosis or prognosis of a cell proliferative disorder, comprising: ~~A method for the analysis of methylation within a nucleic acid molecule comprising Seq. ID No. 1 comprising the following steps;~~

a) obtaining, from a test subject, a biological sample containing genomic DNA,

b) isolating ~~extracting~~ the genomic DNA,

c) digesting the isolated genomic DNA, or a portion thereof, comprising SEQ ID NO:1 ~~Seq. ID No. 1~~ with one or more methylation-sensitive restriction enzymes~~;~~ and

d) determining, by detecting one or more ~~detection~~ of the DNA fragments generated in ~~the digest of step~~ c), the methylation state of at least one CpG dicleotide of SEQ ID NO:1, whereby analysis, diagnosis or prognosis of a cell proliferative disorder is, at least in part, afforded.

27. (Currently amended) The ~~A~~ method of claim 26, further comprising, prior to d), amplification of the DNA digest ~~according to Claim 26, wherein the DNA digest is amplified prior to Step d)~~.

28. (Currently amended) The method of any one of claims 19 or 27, wherein ~~as recited in one of the Claims 19 to 25 and 27 characterised in that~~ more than ten different fragments having a length of about 100 to about 2000 nucleotides ~~100 – 2000 base pairs~~ are amplified.

29. (Currently amended) The method of claim 28, wherein ~~as recited in one of Claims 19 to 25, 27 and 28 characterised in that~~ the amplification ~~of several DNA segments~~ is carried out in one reaction vessel.

30. (Currently amended) The method of any one of claims 19 or 27, wherein ~~as recited in one of the Claims 19 to 25 and 27 to 29, characterised in that~~ the polymerase is a heat-resistant DNA polymerase.

31. (Currently amended) The method of any one of claims 19 or 27, wherein ~~as recited in claims 19 to 25 and 27 to 30, characterised in that~~ the amplification is carried out by ~~means of the~~ polymerase chain reaction (PCR) means.

32. (Currently amended) The method of any one of claims 19 or 27, wherein ~~as recited in one of the Claims 19 to 25 and 27 to 31, characterised in that~~ the amplificates carry detectable labels.

33. (Currently amended) The method of ~~according to~~ Claim 32, wherein the ~~said~~ labels are selected from the group consisting of fluorescence labels, radionuclides, ~~and/or~~ detachable molecule fragments having a typical mass which can be detected in a mass spectrometer, and combinations thereof.

34. (Currently amended) The method of claim 33, wherein ~~as recited in one of the Claims 19 to 25, characterised in that the~~ amplificates or fragments of the amplificates are detected in the mass spectrometer.

35. (Currently amended) The method of claim 34, wherein ~~as recited in one of Claims 33 or 34, characterised in that~~ the produced fragments have a single positive or negative net charge for better detectability in the mass spectrometer.

36. (Currently amended) The method of claim 34, wherein ~~as recited in one of Claims 33 to 35, characterised in that~~ detection is carried out and visualised by means of at least one of matrix assisted laser desorption/ionisation mass spectrometry (MALDI), and ~~or using~~ electron spray mass spectrometry (ESI).

37. (Currently amended) The method of any one of claims 19 and 27, wherein ~~as recited in one of the Claims 19 to 32, characterised in that~~ the genomic DNA is obtained from a source selected from the group consisting of cells or cellular components which contain DNA, ~~sources of DNA comprising, for example,~~ cell lines, histological slides, biopsies, tissue embedded in paraffin, and ~~all possible~~ combinations thereof.

38. (Currently amended) A kit comprising a reagent having at least one of bisulfite, disufite, and hydrogen sulfite, ~~bisulfite (= disulfite, hydrogen sulfite) reagent~~ as well as oligomers or ~~oligonucleotides and/or~~ PNA-oligomers according to any one of the Claims 5 to 13.

39. (Currently amended) The ~~A~~ kit of ~~according to~~ claim 38, further comprising standard reagents for performing a methylation assay from the group consisting of MS-SNuPE, MSP, MethyLight, HeavyMethyl, ~~Methyl light, Heavy Methyl,~~ nucleic acid sequencing, and combinations thereof.

40. (Cancelled) ~~The use of a method according to one of claims 1 to 3, 14, and 19 to 37, a nucleic acid according to Claims 3 to 4, of an oligonucleotide or PNA-oligomer according to one of the Claims 5 to 8, of a kit according to Claim 38 or 39, of an array according to one of the Claims 15 to 18 or of a set of oligonucleotides according to one of claims 9 to 13 for the characterisation, classification, differentiation, grading, staging, and/or diagnosis of cell proliferative disorders, or the predisposition to cell proliferative disorders.~~

41. (Cancelled) ~~The use of a method according to one of claims 1 to 3, 14, and 19 to 37, a nucleic acid according to Claims 3 to 4, of an oligonucleotide or PNA-oligomer according to one of the Claims 5 to 8, of a kit according to Claim 38 or 39, of an array according to one of the Claims 15 to 18 or of a set of oligonucleotides according to one of claims 9 to 13 for the therapy of cell proliferative disorders.~~